AMENDMENTS TO THE CLAIMS

Please amend the claims as follows:

Please cancel claims 1 to 41 and 56 to 92, without prejudice.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Claims 1 to 42 (canceled)

Claim 42 (currently amended): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) a sequence having at least 90% [[70%]] sequence identity to a sequence as set forth in SEQ ID NO: 1, wherein the sequence encodes a polypeptide having amidase activity, and the amidase activity comprises catalysis of the hydrolysis of an amine group in N.alpha.-carbonylbenzyloxy-L-alanine-7-amido-4-methylcoumarin (CBZ-L-ala-AMC); N.alpha.-carbonylbenzyloxy-L-arginine-7-amido-4-methylcoumarin (CBZ-L-arg-AMC); or, N.alpha.-carbonylbenzyloxy-D-arginine-7-amido-4-methylcoumarin (CBZ-D-arg-AMC); or, an activity equivalent to the amidase activity of a polypeptide having a sequence as set forth in SEQ ID NO:2, or, (b) a sequence completely complementary to (a); and

modifying one or more nucleotides in said nucleic acid to another nucleotide, deleting one or more nucleotides in said nucleic acid, or adding one or more nucleotides to said nucleic acid, thereby generating a variant nucleic acid.

Claim 43 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis,

gene reassembly, Gene Site Saturated Mutagenesis™ ~~gene site saturated mutagenesis~~ (GSSM™) and any combination thereof.

Claim 44 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by error-prone PCR.

Claim 45 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by shuffling.

Claim 46 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by oligonucleotide-directed mutagenesis.

Claim 47 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by assembly PCR.

Claim 48 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by sexual PCR mutagenesis.

Claim 49 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by *in vivo* mutagenesis.

Claim 50 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by cassette mutagenesis.

Claim 51 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by recursive ensemble mutagenesis.

Claim 52 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by exponential ensemble mutagenesis.

Claim 53 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by site-specific mutagenesis.

Claim 54 (previously presented): The method of claim 42, wherein the modifications, deletions or additions are introduced by gene reassembly.

Claim 55 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by Gene Site Saturated Mutagenesis™ ~~gene site saturated mutagenesis~~ (GSSM™).

Claims 56 to 92 (canceled)

Claim 93 (currently amended): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) at least 30 consecutive nucleotides of a template sequence having at least 90% [[70%]] sequence identity to a sequence as set forth in SEQ ID NO:1, wherein the template sequence encodes a polypeptide having amidase activity, and the amidase activity comprises an activity equivalent to the amidase activity of a polypeptide having a sequence as set forth in SEQ ID NO:2, or, (b) a sequence completely complementary to (a); and

modifying one or more nucleotides in the nucleic acid to another nucleotide, deleting one or more nucleotides in the nucleic acid, or adding one or more nucleotides to the nucleic acid, thereby generating a variant nucleic acid.

Claim 94 (previously presented): The method of claim 93, wherein the nucleic acid comprises at least 40 consecutive nucleotides.

Claim 95 (previously presented): The method of claim 94, wherein the nucleic acid comprises at least 50 consecutive nucleotides.

Claim 96 (previously presented): The method of claim 95, wherein the nucleic acid comprises at least 75 consecutive nucleotides.

Claim 97 (previously presented): The method of claim 96, wherein the nucleic acid comprises at least 100 consecutive nucleotides.

Claim 98 (previously presented): The method of claim 97, wherein the nucleic acid comprises at least 150 consecutive nucleotides.

Claim 99 (currently amended): The method of claim 93, wherein the modifications, deletions or additions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturated Mutagenesis™ ~~gene site saturated mutagenesis~~ (GSSM™) and any combination thereof.

Claim 100 (currently amended): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) a sequence encoding a polypeptide having an amidase activity, wherein the polypeptide has at least about 90% [[70%]] sequence identity to SEQ ID NO:2, and the amidase activity comprises an activity

equivalent to the amidase activity of a polypeptide having a sequence as set forth in SEQ ID NO:2, or, (b) a sequence completely complementary to (a); and

modifying one or more nucleotides in the nucleic acid to another nucleotide, deleting one or more nucleotides in the nucleic acid, or adding one or more nucleotides to the nucleic acid, thereby generating a variant nucleic acid.

Claim 101 (currently amended): The method of claim 100, wherein the modifications, deletions or additions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturated Mutagenesis™ ~~gene site saturated mutagenesis~~ (GSSM™) and any combination thereof.

Claim 102 (previously presented): The method of claim 42, wherein the sequence has at least 80% sequence identity to a sequence as set forth in SEQ ID NO:1.

Claim 103 (previously presented): The method of claim 102, wherein the sequence has at least 90% sequence identity to a sequence as set forth in SEQ ID NO:1.

Claim 104 (previously presented): The method of claim 103, wherein the sequence has at least 95% sequence identity to a sequence as set forth in SEQ ID NO:1.

Claim 105 (previously presented): The method of claim 104, wherein the sequence is SEQ ID NO:1.

Claim 106 (currently amended): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) a template polynucleotide capable of hybridizing under stringent conditions to a nucleic acid having a sequence as set forth in SEQ ID NO:1, wherein the template sequence encodes a polypeptide having amidase activity, and the amidase activity comprises catalysis of the hydrolysis of an amine group in N.alpha.-carbonylbenzyloxy-L-alanine-7-amido-4-methylcoumarin (CBZ-L-ala-AMC); N.alpha.-carbonylbenzyloxy-L-arginine-7-amido-4-methylcoumarin (CBZ-L-arg-AMC); or, N.alpha.-carbonylbenzyloxy-D-arginine-7-amido-4-methylcoumarin (CBZ-D-arg-AMC); or, an activity equivalent to the amidase activity of a polypeptide having a sequence as set forth in SEQ ID NO:2, or, (b) a sequence completely complementary to (a),

wherein the stringent hybridizing conditions comprise a wash step comprising a wash for 30 minutes at room temperature in a solution comprising 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na_2EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution; and

modifying one or more nucleotides in the nucleic acid to another nucleotide, deleting one or more nucleotides in the nucleic acid, or adding one or more nucleotides to the nucleic acid, thereby generating a variant nucleic acid.

Claim 107 (new): The method of claim 42, wherein the amidase activity comprises catalysis of the hydrolysis of an amine group in N.alpha.-carbonylbenzyloxy-L-alanine-7-amido-4-methylcoumarin (CBZ-L-ala-AMC); N.alpha.-carbonylbenzyloxy-L-arginine-7-amido-4-methylcoumarin (CBZ-L-arg-AMC); or, N.alpha.-carbonylbenzyloxy-D-arginine-7-amido-4-methylcoumarin (CBZ-D-arg-AMC).